This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

As rescanning documents *will not* correct images, please do not report the images to the Image Problem Mailbox.

SEQUENCE LISTING

<110> SYRRX, INC.

<120> CRYSTALLIZATION OF FIBROBLAST ACTIVATION PROTEIN ALPHA (FAPa)

<130> SYR-FAP-5001-C1

<140> Not Yet Assigned
<141> 2003-10-07

<150> 60/417,335
<151> 2002-10-08

<160> 3

<170> PatentIn version 3.1

<210> 1
<211> 760
<212> PRT
<213> Homo sapiens

<220>
<221> Amino acid sequence for full-length human wild type FAPalpha
<222> (1)..(760)
<223>

<300>
<308> Genbank/NP_004451
<309> 2001-11-15
<313> (1)..(760)

<400> 1

```
Met Lys Thr Trp Val Lys Ile Val Phe Gly Val Ala Thr Ser Ala Val
1               5                   10                  15

Leu Ala Leu Leu Val Met Cys Ile Val Leu Arg Pro Ser Arg Val His
            20                  25                  30

Asn Ser Glu Glu Asn Thr Met Arg Ala Leu Thr Leu Lys Asp Ile Leu
        35                  40                  45

Asn Gly Thr Phe Ser Tyr Lys Thr Phe Phe Pro Asn Trp Ile Ser Gly
    50                  55                  60

Gln Glu Tyr Leu His Gln Ser Ala Asp Asn Asn Ile Val Leu Tyr Asn
65                  70                  75                  80

Ile Glu Thr Gly Gln Ser Tyr Thr Ile Leu Ser Asn Arg Thr Met Lys
                85                  90                  95

Ser Val Asn Ala Ser Asn Tyr Gly Leu Ser Pro Asp Arg Gln Phe Val
            100                 105                 110
```

```
Tyr Leu Glu Ser Asp Tyr Ser Lys Leu Trp Arg Tyr Ser Tyr Thr Ala
        115                 120                 125

Thr Tyr Tyr Ile Tyr Asp Leu Ser Asn Gly Glu Phe Val Arg Gly Asn
    130                 135                 140

Glu Leu Pro Arg Pro Ile Gln Tyr Leu Cys Trp Ser Pro Val Gly Ser
145                 150                 155                 160

Lys Leu Ala Tyr Val Tyr Gln Asn Asn Ile Tyr Leu Lys Gln Arg Pro
                165                 170                 175

Gly Asp Pro Pro Phe Gln Ile Thr Phe Asn Gly Arg Glu Asn Lys Ile
            180                 185                 190

Phe Asn Gly Ile Pro Asp Trp Val Tyr Glu Glu Glu Met Leu Ala Thr
        195                 200                 205

Lys Tyr Ala Leu Trp Trp Ser Pro Asn Gly Lys Phe Leu Ala Tyr Ala
    210                 215                 220

Glu Phe Asn Asp Thr Asp Ile Pro Val Ile Ala Tyr Ser Tyr Tyr Gly
225                 230                 235                 240

Asp Glu Gln Tyr Pro Arg Thr Ile Asn Ile Pro Tyr Pro Lys Ala Gly
                245                 250                 255

Ala Lys Asn Pro Val Val Arg Ile Phe Ile Ile Asp Thr Thr Tyr Pro
            260                 265                 270

Ala Tyr Val Gly Pro Gln Glu Val Pro Val Pro Ala Met Ile Ala Ser
        275                 280                 285

Ser Asp Tyr Tyr Phe Ser Trp Leu Thr Trp Val Thr Asp Glu Arg Val
    290                 295                 300

Cys Leu Gln Trp Leu Lys Arg Val Gln Asn Val Ser Val Leu Ser Ile
305                 310                 315                 320

Cys Asp Phe Arg Glu Asp Trp Gln Thr Trp Asp Cys Pro Lys Thr Gln
                325                 330                 335

Glu His Ile Glu Glu Ser Arg Thr Gly Trp Ala Gly Gly Phe Phe Val
            340                 345                 350

Ser Thr Pro Val Phe Ser Tyr Asp Ala Ile Ser Tyr Tyr Lys Ile Phe
        355                 360                 365
```

```
Ser Asp Lys Asp Gly Tyr Lys His Ile His Tyr Ile Lys Asp Thr Val
    370                 375                 380

Glu Asn Ala Ile Gln Ile Thr Ser Gly Lys Trp Glu Ala Ile Asn Ile
385                 390                 395                 400

Phe Arg Val Thr Gln Asp Ser Leu Phe Tyr Ser Ser Asn Glu Phe Glu
                405                 410                 415

Glu Tyr Pro Gly Arg Arg Asn Ile Tyr Arg Ile Ser Ile Gly Ser Tyr
            420                 425                 430

Pro Pro Ser Lys Lys Cys Val Thr Cys His Leu Arg Lys Glu Arg Cys
        435                 440                 445

Gln Tyr Tyr Thr Ala Ser Phe Ser Asp Tyr Ala Lys Tyr Tyr Ala Leu
    450                 455                 460

Val Cys Tyr Gly Pro Gly Ile Pro Ile Ser Thr Leu His Asp Gly Arg
465                 470                 475                 480

Thr Asp Gln Glu Ile Lys Ile Leu Glu Glu Asn Lys Glu Leu Glu Asn
                485                 490                 495

Ala Leu Lys Asn Ile Gln Leu Pro Lys Glu Glu Ile Lys Lys Leu Glu
            500                 505                 510

Val Asp Glu Ile Thr Leu Trp Tyr Lys Met Ile Leu Pro Pro Gln Phe
        515                 520                 525

Asp Arg Ser Lys Lys Tyr Pro Leu Leu Ile Gln Val Tyr Gly Gly Pro
    530                 535                 540

Cys Ser Gln Ser Val Arg Ser Val Phe Ala Val Asn Trp Ile Ser Tyr
545                 550                 555                 560

Leu Ala Ser Lys Glu Gly Met Val Ile Ala Leu Val Asp Gly Arg Gly
                565                 570                 575

Thr Ala Phe Gln Gly Asp Lys Leu Leu Tyr Ala Val Tyr Arg Lys Leu
            580                 585                 590

Gly Val Tyr Glu Val Glu Asp Gln Ile Thr Ala Val Arg Lys Phe Ile
        595                 600                 605

Glu Met Gly Phe Ile Asp Glu Lys Arg Ile Ala Ile Trp Gly Trp Ser
    610                 615                 620
```

```
Tyr Gly Gly Tyr Val Ser Ser Leu Ala Leu Ala Ser Gly Thr Gly Leu
625                 630                 635                 640

Phe Lys Cys Gly Ile Ala Val Ala Pro Val Ser Ser Trp Glu Tyr Tyr
                645                 650                 655

Ala Ser Val Tyr Thr Glu Arg Phe Met Gly Leu Pro Thr Lys Asp Asp
            660                 665                 670

Asn Leu Glu His Tyr Lys Asn Ser Thr Val Met Ala Arg Ala Glu Tyr
        675                 680                 685

Phe Arg Asn Val Asp Tyr Leu Leu Ile His Gly Thr Ala Asp Asp Asn
    690                 695                 700

Val His Phe Gln Asn Ser Ala Gln Ile Ala Lys Ala Leu Val Asn Ala
705                 710                 715                 720

Gln Val Asp Phe Gln Ala Met Trp Tyr Ser Asp Gln Asn His Gly Leu
                725                 730                 735

Ser Gly Leu Ser Thr Asn His Leu Tyr Thr His Met Thr His Phe Leu
            740                 745                 750

Lys Gln Cys Phe Ser Leu Ser Asp
        755                 760
```

```
<210>  2
<211>  2202
<212>  DNA
<213>  Homo sapiens

<220>
<221>  Human cDNA sequence encoding residues 27-760 of FAPa
<222>  (1)..(2202)
<223>

<400>  2
cgcccttcaa gagttcataa ctctgaagaa aatacaatga gagcactcac actgaaggat      60

attttaaatg gaacattttc ttataaaaca ttttttccaa actggatttc aggacaagaa     120

tatcttcatc aatctgcaga taacaatata gtactttata atattgaaac aggacaatca     180

tataccattt tgagtaatag aaccatgaaa agtgtgaatg cttcaaatta cggcttatca     240

cctgatcggc aatttgtata tctagaaagt gattattcaa agctttggag atactcttac     300

acagcaacat attacatcta tgaccttagc aatggagaat ttgtaagagg aaatgagctt     360

cctcgtccaa ttcagtattt atgctggtcg cctgttggga gtaaattagc atatgtctat     420
```

```
caaaacaata tctatttgaa acaaagacca ggagatccac cttttcaaat aacatttaat      480

ggaagagaaa ataaaatatt taatggaatc ccagactggg tttatgaaga ggaaatgctt      540

gctacaaaat atgctctctg gtggtctcct aatggaaaat ttttggcata tgcggaattt      600

aatgatacgg atataccagt tattgcctat tcctattatg gcgatgaaca atatcctaga      660

acaataaata ttccataccc aaaggctgga gctaagaatc ccgttgttcg gatatttatt      720

atcgatacca cttaccctgc gtatgtaggt ccccaggaag tgcctgttcc agcaatgata      780

gcctcaagtg attattattt cagttggctc acgtgggtta ctgatgaacg agtatgtttg      840

cagtggctaa aaagagtcca gaatgtttcg gtcctgtcta tatgtgactt cagggaagac      900

tggcagacat gggattgtcc aaagacccag gagcatatag aagaaagcag aactggatgg      960

gctggtggat tctttgtttc aacaccagtt ttcagctatg atgccatttc gtactacaaa     1020

atatttagtg acaaggatgg ctacaaacat attcactata tcaaagacac tgtggaaaat     1080

gctattcaaa ttacaagtgg caagtgggag gccataaata tattcagagt aacacaggat     1140

tcactgtttt attctagcaa tgaatttgaa gaataccctg gaagaagaaa catctacaga     1200

attagcattg gaagctatcc tccaagcaag aagtgtgtta cttgccatct aaggaaagaa     1260

aggtgccaat attacacagc aagtttcagc gactacgcca agtactatgc acttgtctgc     1320

tacggcccag gcatccccat ttccacccttt catgatggac gcactgatca agaaattaaa     1380

atcctggaag aaaacaagga attggaaaat gctttgaaaa atatccagct gcctaaagag     1440

gaaattaaga aacttgaagt agatgaaatt actttatggt acaagatgat tcttcctcct     1500

caatttgaca gatcaaagaa gtatcccttg ctaattcaag tgtatggtgg tccctgcagt     1560

cagagtgtaa ggtctgtatt tgctgttaat tggatatctt atcttgcaag taaggaaggg     1620

atggtcattg ccttggtgga tggtcgagga acagctttcc aaggtgacaa actcctctat     1680

gcagtgtatc gaaagctggg tgtttatgaa gttgaagacc agattacagc tgtcagaaaa     1740

ttcatagaaa tgggtttcat tgatgaaaaa agaatagcca tatggggctg gtcctatgga     1800

ggatacgttt catcactggc ccttgcatct ggaactggtc ttttcaaatg tggtatagca     1860

gtggctccag tctccagctg ggaatattac gcgtctgtct acacagagag attcatgggt     1920

ctcccaacaa aggatgataa tcttgagcac tataagaatt caactgtgat ggcaagagca     1980

gaatatttca gaaatgtaga ctatcttctc atccacggaa cagcagatga taatgtgcac     2040

tttcaaaact cagcacagat tgctaaagct ctggttaatg cacaagtgga tttccaggca     2100

atgtggtact ctgaccagaa ccacggctta tccggcctgt ccacgaacca cttatacacc     2160

cacatgaccc acttcctaaa gcagtgtttc tctttgtcag ac                        2202

<210>  3
<211>  744
```

<212> PRT
<213> Homo sapiens

<220>
<221> Amino acid sequence for residues 27-760 of FAP alpha
<222> (1)..(744)
<223>

<220>
<221> Amino acid sequence for residues 27-760 of FAP alpha
<222> (1)..(744)
<223> includes N-terminal signal sequence (ADPG) and C-terminal 6 histidine tag

<400> 3

```
Ala Asp Pro Gly Arg Pro Ser Arg Val His Asn Ser Glu Glu Asn Thr
1               5                   10                  15

Met Arg Ala Leu Thr Leu Lys Asp Ile Leu Asn Gly Thr Phe Ser Tyr
            20                  25                  30

Lys Thr Phe Phe Pro Asn Trp Ile Ser Gly Gln Glu Tyr Leu His Gln
        35                  40                  45

Ser Ala Asp Asn Asn Ile Val Leu Tyr Asn Ile Glu Thr Gly Gln Ser
    50                  55                  60

Tyr Thr Ile Leu Ser Asn Arg Thr Met Lys Ser Val Asn Ala Ser Asn
65                  70                  75                  80

Tyr Gly Leu Ser Pro Asp Arg Gln Phe Val Tyr Leu Glu Ser Asp Tyr
                85                  90                  95

Ser Lys Leu Trp Arg Tyr Ser Tyr Thr Ala Thr Tyr Tyr Ile Tyr Asp
            100                 105                 110

Leu Ser Asn Gly Glu Phe Val Arg Gly Asn Glu Leu Pro Arg Pro Ile
        115                 120                 125

Gln Tyr Leu Cys Trp Ser Pro Val Gly Ser Lys Leu Ala Tyr Val Tyr
    130                 135                 140

Gln Asn Asn Ile Tyr Leu Lys Gln Arg Pro Gly Asp Pro Pro Phe Gln
145                 150                 155                 160

Ile Thr Phe Asn Gly Arg Glu Asn Lys Ile Phe Asn Gly Ile Pro Asp
                165                 170                 175

Trp Val Tyr Glu Glu Glu Met Leu Ala Thr Lys Tyr Ala Leu Trp Trp
            180                 185                 190
```

```
Ser Pro Asn Gly Lys Phe Leu Ala Tyr Ala Glu Phe Asn Asp Thr Asp
        195                 200                 205

Ile Pro Val Ile Ala Tyr Ser Tyr Tyr Gly Asp Glu Gln Tyr Pro Arg
    210                 215                 220

Thr Ile Asn Ile Pro Tyr Pro Lys Ala Gly Ala Lys Asn Pro Val Val
225                 230                 235                 240

Arg Ile Phe Ile Ile Asp Thr Thr Tyr Pro Ala Tyr Val Gly Pro Gln
                245                 250                 255

Glu Val Pro Val Pro Ala Met Ile Ala Ser Ser Asp Tyr Tyr Phe Ser
            260                 265                 270

Trp Leu Thr Trp Val Thr Asp Glu Arg Val Cys Leu Gln Trp Leu Lys
        275                 280                 285

Arg Val Gln Asn Val Ser Val Leu Ser Ile Cys Asp Phe Arg Glu Asp
    290                 295                 300

Trp Gln Thr Trp Asp Cys Pro Lys Thr Gln Glu His Ile Glu Glu Ser
305                 310                 315                 320

Arg Thr Gly Trp Ala Gly Gly Phe Phe Val Ser Thr Pro Val Phe Ser
                325                 330                 335

Tyr Asp Ala Ile Ser Tyr Tyr Lys Ile Phe Ser Asp Lys Asp Gly Tyr
            340                 345                 350

Lys His Ile His Tyr Ile Lys Asp Thr Val Glu Asn Ala Ile Gln Ile
        355                 360                 365

Thr Ser Gly Lys Trp Glu Ala Ile Asn Ile Phe Arg Val Thr Gln Asp
    370                 375                 380

Ser Leu Phe Tyr Ser Ser Asn Glu Phe Glu Glu Tyr Pro Gly Arg Arg
385                 390                 395                 400

Asn Ile Tyr Arg Ile Ser Ile Gly Ser Tyr Pro Pro Ser Lys Lys Cys
                405                 410                 415

Val Thr Cys His Leu Arg Lys Glu Arg Cys Gln Tyr Tyr Thr Ala Ser
            420                 425                 430

Phe Ser Asp Tyr Ala Lys Tyr Tyr Ala Leu Val Cys Tyr Gly Pro Gly
```

```
        435                 440                 445

Ile Pro Ile Ser Thr Leu His Asp Gly Arg Thr Asp Gln Glu Ile Lys
    450                 455                 460

Ile Leu Glu Glu Asn Lys Glu Leu Glu Asn Ala Leu Lys Asn Ile Gln
465                 470                 475                 480

Leu Pro Lys Glu Glu Ile Lys Lys Leu Glu Val Asp Glu Ile Thr Leu
                485                 490                 495

Trp Tyr Lys Met Ile Leu Pro Pro Gln Phe Asp Arg Ser Lys Lys Tyr
            500                 505                 510

Pro Leu Leu Ile Gln Val Tyr Gly Gly Pro Cys Ser Gln Ser Val Arg
        515                 520                 525

Ser Val Phe Ala Val Asn Trp Ile Ser Tyr Leu Ala Ser Lys Glu Gly
    530                 535                 540

Met Val Ile Ala Leu Val Asp Gly Arg Gly Thr Ala Phe Gln Gly Asp
545                 550                 555                 560

Lys Leu Leu Tyr Ala Val Tyr Arg Lys Leu Gly Val Tyr Glu Val Glu
                565                 570                 575

Asp Gln Ile Thr Ala Val Arg Lys Phe Ile Glu Met Gly Phe Ile Asp
            580                 585                 590

Glu Lys Arg Ile Ala Ile Trp Gly Trp Ser Tyr Gly Gly Tyr Val Ser
        595                 600                 605

Ser Leu Ala Leu Ala Ser Gly Thr Gly Leu Phe Lys Cys Gly Ile Ala
    610                 615                 620

Val Ala Pro Val Ser Ser Trp Glu Tyr Tyr Ala Ser Val Tyr Thr Glu
625                 630                 635                 640

Arg Phe Met Gly Leu Pro Thr Lys Asp Asp Asn Leu Glu His Tyr Lys
                645                 650                 655

Asn Ser Thr Val Met Ala Arg Ala Glu Tyr Phe Arg Asn Val Asp Tyr
            660                 665                 670

Leu Leu Ile His Gly Thr Ala Asp Asp Asn Val His Phe Gln Asn Ser
        675                 680                 685
```

```
Ala Gln Ile Ala Lys Ala Leu Val Asn Ala Gln Val Asp Phe Gln Ala
    690                 695                 700

Met Trp Tyr Ser Asp Gln Asn His Gly Leu Ser Gly Leu Ser Thr Asn
705                 710                 715                 720

His Leu Tyr Thr His Met Thr His Phe Leu Lys Gln Cys Phe Ser Leu
                725                 730                 735

Ser Asp His His His His His His
            740
```